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NETAFFX™ ANALYSIS CENTER

Details for HG-U95AV2:36809_AT

Full Screen

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GeneChip Array Information

Probe Set ID	36809_at
GeneChip Array	Human Genome U95Av2 Array
Organism	Human
Common Name	

Probe Design Information

Transcript ID (Array Design)	4849545
Sequence Type	Consensus sequence
Representative Public ID	L01664 NCBI
Archival UniGene Cluster	Hs.889 NCBI
Target Description	Cluster Incl. L01664:Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) mRNA, complete cds /cds=(33,461) /gb=L01664 /gi=187273 /ug=Hs.889 /len=586

Annotation Method Description

Annotation Description	36809_at was annotated using the Matching Probes based pipeline to a Entrez Gene identifier using 6 transcript(s).
Annotation Grade	This is a grade A annotation.
Annotation Transcript Cluster (# of Matching Probes)	BC119711(16), BC119712(16), ENST00000221804(15), ENST00000392050(14), L01664(16), NM_001828(15)

	Representative Transcript	Description	Matching Probes	Related Probesets by Grade
Transcript Assignments	BC119711 NCBI	Homo sapiens Charcot-Leyden crystal protein, mRNA (cDNA clone MGC:149659 IMAGE:40117193), complete cds.	16/16	None
	BC119712 NCBI	Homo sapiens Charcot-Leyden crystal protein, mRNA (cDNA clone MGC:149660 IMAGE:40117194), complete cds.	16/16	None
	ENST00000221804 Ensembl	Eosinophil lysophospholipase gene: ENSG00000105205	15/16	None
	ENST00000392050 Ensembl	Uncharacterized protein CLC (Fragment) gene:ENSG00000105205	14/16	None

GENSCAN00000021248 Ensembl	cdna:Genscan chromosome: NCBI36:19:44908625:44920939:-1	13/16	None
L01664 NCBI	Homo sapiens Charcot-Leyden crystal protein mRNA, complete cds.	16/16	None
NM_001828 NCBI	Homo sapiens Charcot-Leyden crystal protein (CLC), mRNA.	15/16	None
uc002omh.1 UCSC		15/16	None

Annotation Notes There are no noteworthy cross hybridizing mRNAs found for this probe set.

Genomic Alignment of Consensus/Exemplar Sequence

Assembly	March 2006 (NCBI Build 36.1)				
Alignment(s)	Position	View using IGB	Identity	Coverage	Cytoband
	chr19:44913857-44917553(-) UCSC ENSEMBL	IGB *	88.84	88.8	q13.2
* You can now view alignments using the Integrated Genome Browser (IGB) . Note that you must start IGB before clicking on any of the "IGB" links above.					

Public Domain and Genome References

Gene Title	Charcot-Leyden crystal protein
Gene Symbol	CLC HGNC
Chromosomal Location	19q13.1
UniGene ID Build 212 (11 Apr 2008)	Hs.889 NCBI (FULL LENGTH)
Ensembl	ENSG00000105205
Entrez Gene ID	1178 Entrez gene
SwissProt	A8MXT7 EMBL-EBI Q05315 EMBL-EBI
EC	3.1.1.5
OMIM	153310 NCBI
RefSeq Protein ID	NP_001819.2 NCBI
RefSeq	RefSeq Transcript ID RefSeq Title NM_001828 NCBI

Functional Annotations

Gene Ontology	GO Biological Process (view graph)			
	ID	Description	Evidence	Links
	0006644	phospholipid metabolic process	not recorded	QuickGO AmiGO
	0007275	multicellular organismal development	traceable author statement	QuickGO AmiGO
	0016042	lipid catabolic process	inferred from electronic annotation	QuickGO AmiGO
	GO Molecular Function (view graph)			
	ID	Description	Evidence	Links
	0004091	carboxylesterase activity	inferred from electronic annotation	QuickGO AmiGO
	0004622	lysophospholipase activity	inferred from electronic annotation	QuickGO AmiGO
	0005529	sugar binding	inferred from electronic annotation	QuickGO AmiGO
	0016787	hydrolase activity	inferred from electronic annotation	QuickGO AmiGO

Sequence					
Target Sequence	<p>>HG-U95AV2 : 36809_AT</p> <pre>ctaccCGTgCCatAcacagaggCtgcCTcTTtgTctactggTtctactgtGacaatcaaa ggcgaccactTgtctgtttcttgaatgaaccatatctgcaggtggatttcacactgag atgaaggaggaatcagacattgtcttccatttccaagtgtgctttggTcgtcgtgtggTc atgaacagccgtgagt atggggcctggaagcagcaggtggaatccaagaacatgccctt cagnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnctgccagataagtaccaggtaatg gtcaatggccaatcctcttacacctttgaccatagaatcaagcctgaggctgtgaagatg gtgcaagtgtggagagatatctccctgaccaaatttaatgtcagctatttaaagagataa cc</pre> <p><u>BLASTn GenBank NR</u></p> <p>Note: "n"s represent regions that are not probed by the probe sequences.</p>				
Probe Info	Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Target Strandedness
	CTACCCGTGCCATACACAGAGGCTG	334	293	57	Antisense
	GTGCCATACACAGAGGCIGCCTCTT	317	33	63	Antisense
	AATGAACCATATCTGCAGGTGGATT	237	207	141	Antisense
	TTCACACTGAGATGAAGGAGGAAT	67	205	165	Antisense
	CCCACTGAGATGAAGGAGGAATCA	149	151	167	Antisense
	GACATTGCTCTTCCATTTCGAAGTGT	184	77	192	Antisense
	CCTCGTGTTGGTCATGAACAGCCGTG	349	129	225	Antisense
	GTGGTCATGAACAGCCGTGAGTATG	181	529	231	Antisense
	ATGAACAGCCGTGAGTATGGGGCCT	96	325	237	Antisense
	CCITGAAGCAGCAGGTGGAATCCAA	26	227	259	Antisense
	GGAATCCAAGAACATGCCCTTTCAG	533	157	275	Antisense
	CTGCCAGATAAGTACCAGGTAATGG	220	353	333	Antisense
	ACCTTTGACCATAGAATCAAGCCTG	97	49	378	Antisense
	GAATCAAGCCTGAGGCTGTGAAGAT	501	41	391	Antisense
	TGGAGAGATATCTCCCTGACCAAAT	15	507	426	Antisense
	ATGTCAGCTATTTAAAGAGATAACC	341	19	454	Antisense
Sequence Source	GenBank				